Appendix III: Alignment of intron A of M60321 with instant SEQ ID NO: 3

```
BLASTN 2.2.25+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.


RID: N069FRCK111


Query= gi|330624|gb|M60321.1|HS5MIEP Human cytomegalovirus major
immediate-early protein gene, 5' end

Length=2361
```

| | Score | E |
| Sequences producing significant alignments: | (Bits) | Value |

```
lcl|35151  SID_3                                      630    0.0

ALIGNMENTS
>lcl|35151 SID_3
Length=3584

 Score =  630 bits (341),  Expect = 0.0
 Identities = 349/353 (99%), Gaps = 1/353 (0%)
 Strand=Plus/Plus

Query  1737   TCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCACAATGCCC   1796
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1010   TCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCACAATGCCC   1069

Query  1797   ACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAAATGAGCTC   1856
              ||||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||||
Sbjct  1070   ACCACCACCAGTGTGCCACACAAGGCCGWGGCGGTAGGGTATGTGTCTGAAAATGAGCTC   1129

Query  1857   GGAGATTGGGCTCGCACCG-TGACGCAGATGGAAGACTTAAGGCAGCGGCAGAAGAAGAT   1915
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1130   GGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAGAAGAAGAT   1189

Query  1916   GCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGCGGTGCTG   1975
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1190   GCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGCGGTGCTG   1249

Query  1976   TTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGA   2035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1250   TTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGA   1309

Query  2036   CATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAG     2088
              ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  1310   CATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTTTTTTCTGCAG     1362


 Score =  449 bits (243),  Expect = 1e-129
 Identities = 248/250 (99%), Gaps = 1/250 (0%)
 Strand=Plus/Plus

Query  1265   GTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCATGCTATACTG   1324
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  760    GTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCATGCTATACTG   819
```

```
Query  1325  TTTTTGGCTTGGGGCCTATACACCCCCGCT-CCTTATGCTATAGGTGATGGTATAGCTTA  1383
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  820   TTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGGTGATGGTATAGCTTA  879

Query  1384  GCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATTGGTGACGATACTTTC  1443
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  880   GCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATTGGTGACGATACTTTC  939

Query  1444  CATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTGGCTATATGCCAATA  1503
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  940   CATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTGGCTATATGCCAATA  999

Query  1504  CTCTGTCCTT    1513
             | |||||||||
Sbjct  1000  CACTGTCCTT    1009
```